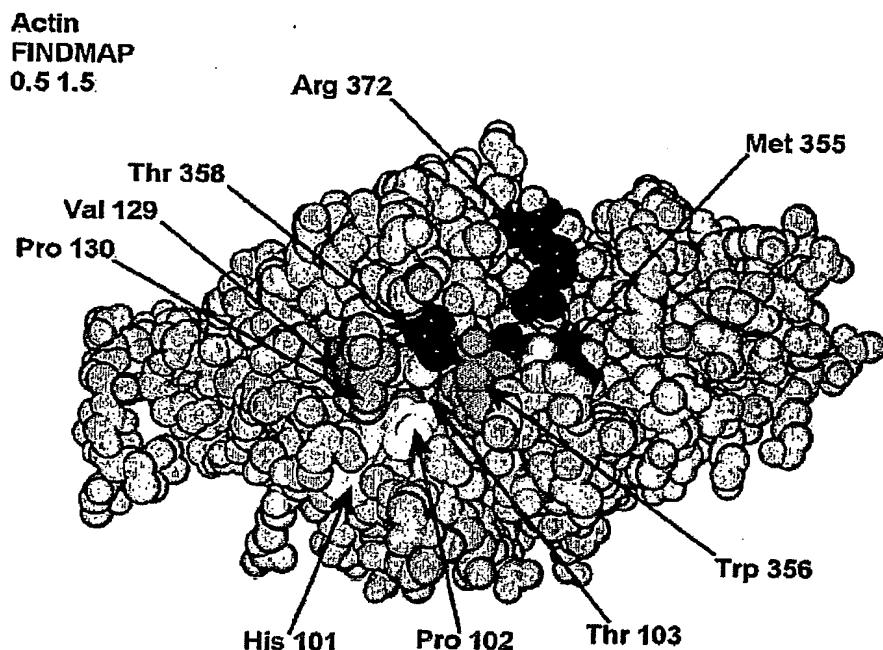


		target residue																				
		A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y	-
probe residue	A	1	0	0	0	0	0.5	0	0	0.5	0	0	0	0.5	0	0	0.5	0.25	0	0	0	-1
	C		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	-1
	D			1	0.5	0	0	0	0	0	0	0.5	0	0.25	0	0	0	0	0	0	0	-1
	E				1	0	0	0	0	0	0	0.25	0	0.5	0	0	0	0	0	0	0	-1
	F					1	0	0	0	0	0	0	0	0	0	0	0	0	0	0.25	0.5	-1
	G						1	0	0	0	0	0	0.5	0.5	0	0	0.25	0.25	0	0	0	-1
	H							1	0	0.25	0	0	0	0	0	0.25	0	0	0	0	0	-1
	I								1	0	0.5	0.25	0	0	0	0	0	0	0.5	0	0	-1
	K									1	0	0	0	0	0.5	0.5	0	0.5	0	0	0	-1
	L										1	0.25	0	0	0	0	0	0	0.5	0	0	-1
	M											1	0	0	0	0	0	0.25	0	0	0	-1
	N												1	0	0.25	0	0	0	0	0	0	-1
	P												1	0	0	0	0	0	0	0	0	-1
	Q													1	0	0	0	0	0	0	0	-1
	R														1	0	0	0	0	0	0	-1
	S															1	0.5	0	0	0	0	-1
	T																1	0	0	0	0	-1
	V																	1	0	0	0	-1
	W																		1	0.25	-1	
	Y																			1	-1	

FIGURE 1



DEDETTALVCDNGSGLVKA##### 1-70

345

12

HPT

VP

YNELRVAPEEEHPTLLTEAPLNPKANREKMTQIMFETFNVPA MYVAIQAVL 71-140

SLIYASGRTTGIVLDSDGVTHNVP IYEGYALPHAIMRLDLAGRDLTDYL##### 141-210

211-280

APPERKYSVWIGGSILASLS 281-350

76
MW
TFQQMWITKQEYDEAGPSIVHR 351-372

8
R

FIGURE 2

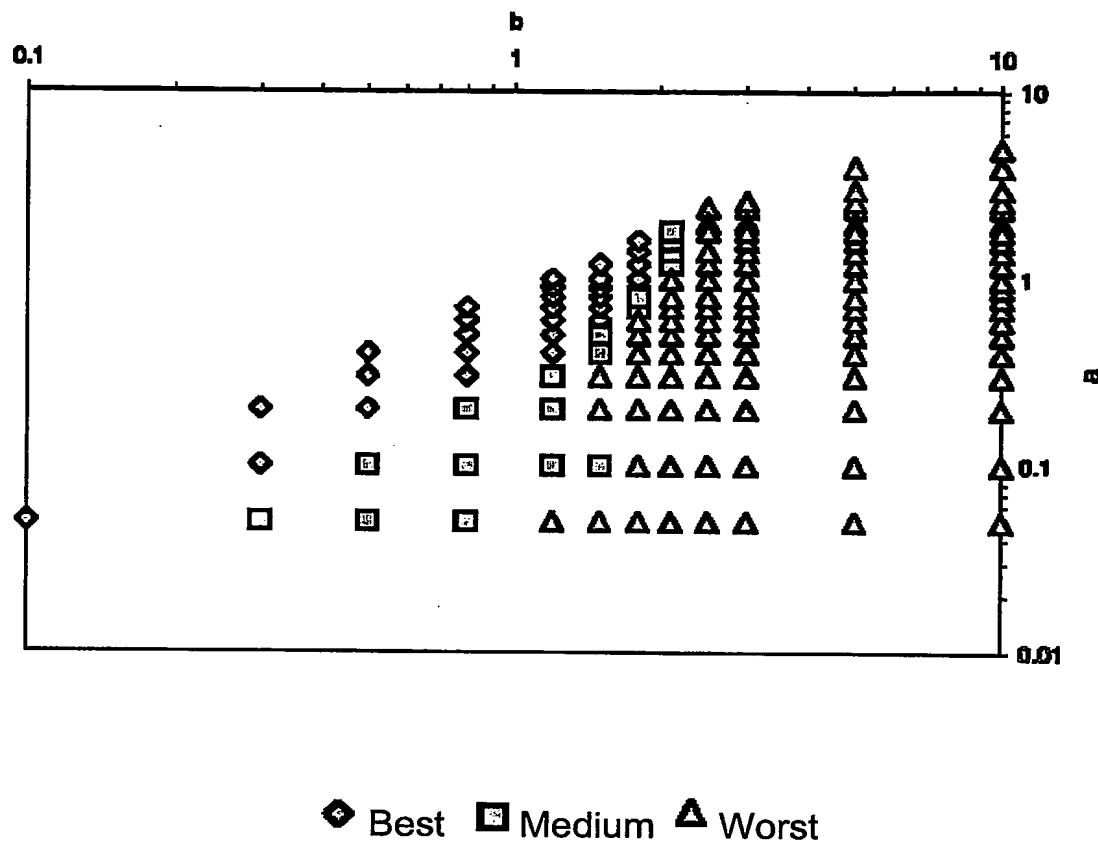


FIGURE 3

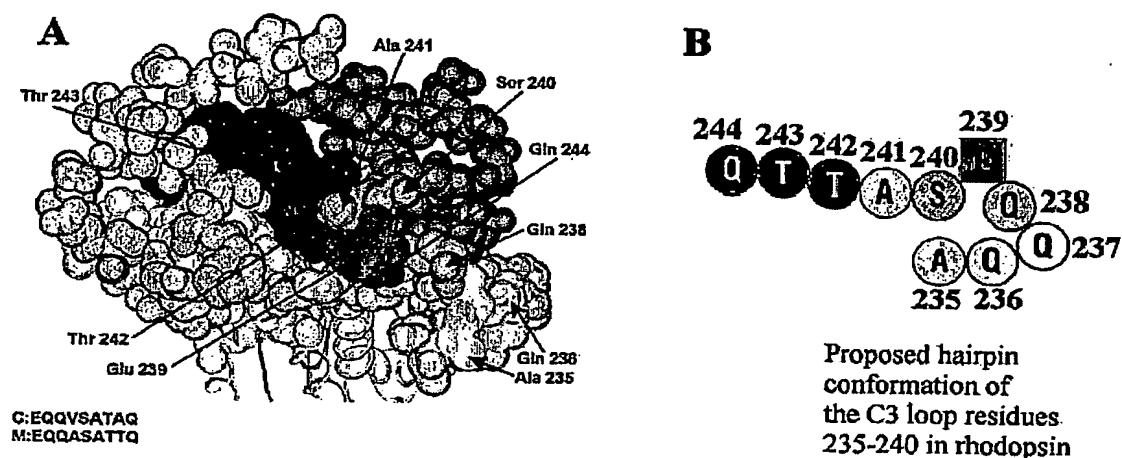


FIGURE 4

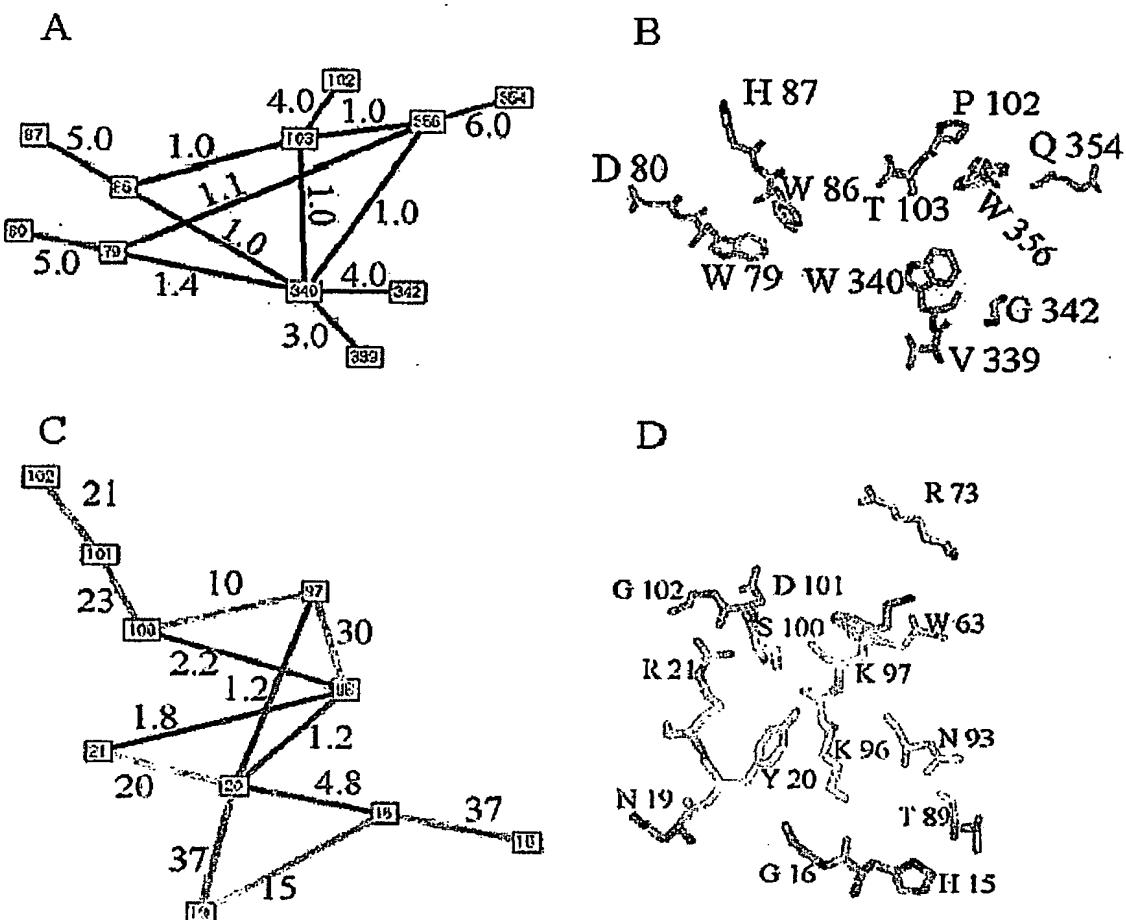


FIGURE 5